MEAN SIMILARITY OUTPUT MATRICES FOR:

McCormick, F.H., D.V. Peck, and D.P. Larsen. 2000. Comparison of geographic classification schemes for Mid-Atlantic stream fish assemblages. Journal of the North American Benthological Society 19(3):385-404.

The following pages represent the results of mean similarity analyses conducted using the software package MEANSIM6.

RESULTS FOR TAXONOMIC CLUSTERS: ALL SITES

BRAY-CURTIS DISSIMILARITY COEFFICIENT

```
Cluster Descriptions:

BC1:  predominantly blacknose dace
BC2:  predominantly brook trout
BC3:  predominantly creek chub
BC4:  blacknose dace + creek chub
BC5:  predominantly blacknose dace + white sucker + longnose dace + other species
BC6:  predominantly slimy sculpin + brook trout + white sucker + other species
BC7:  white sucker + stoneroller + rock bass + blacknose dace + other taxa
BC8:  white sucker + blacknose dace + creek chub + longnose dace + other taxa


 Run ID = Bray-Curtis similarity: Clusters (B-C dissimilarity) (9/99)
 Number of sites = 200


 Groups =  BC1       BC8         BC5        BC3        BC2         BC6       BC4     BC7
 Sizes  =   35        30          49          8          7           9        12      50

 Matrix of mean similarities:
             BC1     BC8     BC5     BC3     BC2     BC6     BC4     BC7
      BC1   0.802   0.233   0.463   0.052   0.060   0.018   0.356   0.043
      BC8   0.000   0.322   0.323   0.139   0.078   0.131   0.332   0.144
      BC5   0.000   0.000   0.507   0.133   0.153   0.070   0.429   0.113
      BC3   0.000   0.000   0.000   0.505   0.043   0.044   0.445   0.056
      BC2   0.000   0.000   0.000   0.000   0.527   0.102   0.090   0.039
      BC6   0.000   0.000   0.000   0.000   0.000   0.588   0.049   0.054
      BC4   0.000   0.000   0.000   0.000   0.000   0.000   0.694   0.075
      BC7   0.000   0.000   0.000   0.000   0.000   0.000   0.000   0.149

 Number of between and within similarities =  16318  3582

 Weighted within-groups mean similarity, Wbar =    0.457
 Unweighted within-groups mean =    0.415
 Between-groups mean similarity, Bbar = 0.186

 Observed ratio, M = Bbar/Wbar = 0.407
 Observed difference, (Wbar-Bbar) = 0.271

 Permutation test not done.
```

These results are summarized in Figure 2A of the manuscript.

RESULTS FOR TAXONOMIC CLUSTERS: ALL SITES

DICE-SØRENSEN DISSIMILARITY COEFFICIENT

```
Cluster descriptions:

DS1:  predominantly blacknose dace
DS2:  predominantly blacknose dace and creek chub
DS3:  white sucker + creek chub + blacknose dace + other taxa
DS4:  brook trout + 1 or 2 other species
DS5:  predominantly creek chub
DS6:  predominantly brook trout and slimy sculpin
DS7:  blacknose dace + fantail darter + other taxa
DS8:  white sucker + stoneroller + blacknose dace + other taxa

 Run ID = Dice (Sorensen) similarity: Clusters (Dice dissimilarity) (9/99)
 Number of sites = 200


 Groups =   1          7          3          6          4          2          8
5
 Sizes  =  14         25         74         11          7         17         48
4

 Matrix of mean similarities:
               1       7       3       6       4       2       8       5
       1   0.782   0.358   0.234   0.002   0.012   0.520   0.107   0.000
       7   0.000   0.413   0.326   0.217   0.130   0.326   0.206   0.000
       3   0.000   0.000   0.491   0.213   0.075   0.413   0.329   0.232
       6   0.000   0.000   0.000   0.294   0.148   0.109   0.146   0.089
       4   0.000   0.000   0.000   0.000   0.174   0.034   0.067   0.000
       2   0.000   0.000   0.000   0.000   0.000   0.789   0.148   0.567
       8   0.000   0.000   0.000   0.000   0.000   0.000   0.338   0.048
       5   0.000   0.000   0.000   0.000   0.000   0.000   0.000   1.000

 Number of between and within similarities =  15462  4438

 Weighted within-groups mean similarity, Wbar =    0.478
 Unweighted within-groups mean =    0.458
 Between-groups mean similarity, Bbar = 0.253

 Observed ratio, M = Bbar/Wbar = 0.529
 Observed difference, (Wbar-Bbar) = 0.225

 Permutation test not done.
```

These results are summarized in Figure 2A of the manuscript.

RESULTS FOR ECOREGION GROUPS: ALL SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

Ecoregion groups:

BLUE RDG: Blue Ridge
C. APPS: Central Appalachian Plateau
L-D VAL: Limestone-dolomite valleys
N. APPS: Allegheny Plateau
PIEDMONT: Piedmont
SND RDG: Sandstone ridges
SHL RDG: Shale Ridges
SHL VAL: Shale valleys
W. APPS: Western Appalachian Plateau

Run ID = Bray-Curtis similarity: Ecoregion groups (9/99)
Number of sites = 200

Groups =	C. APPS	SHL RDG	L-D VAL	PIEDMONT	SND RDG	N. APPS	SHL VAL	W. APPS	BLUE RDG
Sizes =	13	21	54	14	19	9	52	11	7

Matrix of mean similarities:

	C. APPS	SHL RDG	L-D VAL	PIEDMONT	SND RDG	N. APPS	SHL VAL	W. APPS	BLUE RDG
C. APPS	0.145	0.205	0.156	0.118	0.174	0.158	0.193	0.220	0.173
SHL RDG	0.000	0.304	0.253	0.205	0.273	0.226	0.292	0.241	0.280
L-D VAL	0.000	0.000	0.225	0.179	0.218	0.186	0.239	0.202	0.213
PIEDMONT	0.000	0.000	0.000	0.223	0.188	0.148	0.206	0.166	0.234
SND RDG	0.000	0.000	0.000	0.000	0.217	0.195	0.245	0.196	0.247
N. APPS	0.000	0.000	0.000	0.000	0.000	0.216	0.228	0.257	0.148
SHL VAL	0.000	0.000	0.000	0.000	0.000	0.000	0.273	0.265	0.240
W. APPS	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.398	0.164
BLUE RDG	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.269

Number of between and within similarities = 16481 3419

Weighted within-groups mean similarity, Wbar = 0.250
Unweighted within-groups mean = 0.249
Between-groups mean similarity, Bbar = 0.223

Observed ratio, M = Bbar/Wbar = 0.890
Observed difference, (Wbar-Bbar) = 0.276E-01

Starting 10000 randomly-sampled permutations.
Random Seed = -936915417

Random-sampling permutation test finished

Number of random trials = 10000

Number of trials with [M < (Observed M)] = 0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] = 0
For (Wbar-Bbar), estimated P-value =< 0.0001

These results are summarized in Figure 2B of the manuscript.

RESULTS FOR ECOREGION GROUPS: ALL SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

Ecoregion groups:

BLUE RDG: Blue Ridge
C. APPS: Central Appalachian Plateau
L-D VAL: Limestone-dolomite valleys
N. APPS: Allegheny Plateau
PIEDMONT: Piedmont
SND RDG: Sandstone ridges
SHL RDG: Shale Ridges
SHL VAL: Shale valleys
W. APPS: Western Appalachian Plateau

Run ID = Dice (Sorensen) similarity: Ecoregion Groups (9/99)
Number of sites = 200

Groups = C. APPS SHL RDG L-D VAL PIEDMONT SND RDG N. APPS SHL VAL W. APPS BLUE RDG
Sizes = 13 21 54 14 19 9 52 11 7

Matrix of mean similarities:

	C. APPS	SHL RDG	L-D VAL	PIEDMONT	SND RDG	N. APPS	SHL VAL	W. APPS	BLUE RDG
C. APPS	0.196	0.266	0.226	0.154	0.217	0.202	0.249	0.288	0.237
SHL RDG	0.000	0.356	0.332	0.260	0.306	0.294	0.350	0.333	0.316
L-D VAL	0.000	0.000	0.321	0.257	0.272	0.263	0.325	0.309	0.271
PIEDMONT	0.000	0.000	0.000	0.342	0.249	0.231	0.288	0.250	0.263
SND RDG	0.000	0.000	0.000	0.000	0.263	0.281	0.296	0.276	0.265
N. APPS	0.000	0.000	0.000	0.000	0.000	0.312	0.292	0.299	0.222
SHL VAL	0.000	0.000	0.000	0.000	0.000	0.000	0.351	0.341	0.298
W. APPS	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.427	0.307
BLUE RDG	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.302

Number of between and within similarities = 16481 3419

Weighted within-groups mean similarity, Wbar = 0.325
Unweighted within-groups mean = 0.331
Between-groups mean similarity, Bbar = 0.292

Observed ratio, M = Bbar/Wbar = 0.899
Observed difference, (Wbar-Bbar) = 0.329E-01

Starting 10000 randomly-sampled permutations.
Random Seed = -936915032

Random-sampling permutation test finished

Number of random trials = 10000

Number of trials with [M < (Observed M)] = 0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] = 0
For (Wbar-Bbar), estimated P-value =< 0.0001

These results are summarized in Figure 2B of the manuscript.

RESULTS FOR CATCHMENTS (Modified HUCs): ALL SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

Catchment descriptions:

DELAWARE: Delaware R.

CHES.-PO: Middle Chesapeake Bay and the Potomac R.
L. CHES.: Lower Chesapeake Bay (incl. the York, Rappahannock, and James rivers)
UP. OHIO: Upper Ohio R. (including the Allegheny, Monongehela, Youghigheny, and Cheat rivers
and small tributaries to the upper Ohio River mainstem)
L. OHIO: Lower Ohio R. (incl. the Kanawha and Big Sandy rivers)
ROANCHOW: Roanoke and Chowan rivers
SUSQUEHA: Susquehanna R.
UP. TENN: Upper Tennessee River

Run ID = Bray-Curtis similarity: HUC groups (9/99)
Number of sites = 200

Groups =	UP. OHIO	CHES.-PO	SUSQUEHA	DELAWARE	L. CHES.	ROANCHOW	L. OHIO	UP. TENN
Sizes =	19	51	48	11	20	10	27	14

Matrix of mean similarities:

	UP. OHIO	CHES.-PO	SUSQUEHA	DELAWARE	L. CHES.	ROANCHOW	L. OHIO	UP. TENN
UP. OHIO	0.307	0.233	0.242	0.251	0.209	0.142	0.212	0.165
CHES.-PO	0.000	0.273	0.255	0.283	0.284	0.142	0.210	0.175
SUSQUEHA	0.000	0.000	0.278	0.320	0.249	0.122	0.190	0.178
DELAWARE	0.000	0.000	0.000	0.388	0.275	0.123	0.195	0.174
L. CHES.	0.000	0.000	0.000	0.000	0.382	0.174	0.222	0.167
ROANCHOW	0.000	0.000	0.000	0.000	0.000	0.173	0.141	0.094
L. OHIO	0.000	0.000	0.000	0.000	0.000	0.000	0.183	0.161
UP. TENN	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.193

Number of between and within similarities = 16594 3306

Weighted within-groups mean similarity, Wbar = 0.272
Unweighted within-groups mean = 0.272
Between-groups mean similarity, Bbar = 0.218

Observed ratio, M = Bbar/Wbar = 0.803
Observed difference, (Wbar-Bbar) = 0.537E-01

Starting 10000 randomly-sampled permutations.
Random Seed = -936915477

Random-sampling permutation test finished

Number of random trials = 10000

Number of trials with [M < (Observed M)] = 0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] = 0
For (Wbar-Bbar), estimated P-value =< 0.0001

These results are summarized in Figure 2C of the manuscript.

RESULTS FOR CATCHMENTS (Modified HUCs): ALL SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

Catchment descriptions:

CHES.-PO: Middle Chesapeake Bay and the Potomac R.
L. CHES.: Lower Chesapeake Bay (incl. the York, Rappahannock, and James rivers)
UP. OHIO: Upper Ohio R. (including the Allegheny, Monongehela, Youghigheny, and Cheat rivers
and small tributaries to the upper Ohio River mainstem)
L. OHIO: Lower Ohio R. (incl. the Kanawha and Big Sandy rivers)
ROANCHOW: Roanoke and Chowan rivers
SUSQUEHA: Susquehanna R.
UP. TENN: Upper Tennessee River

Run ID = Dice (Sorensen) similarity: HUC groups (9/99)
Number of sites = 200

Groups =	UP. OHIO	CHES.-PO	SUSQUEHA	DELAWARE	L. CHES.	ROANCHOW	L. OHIO	UP. TENN
Sizes =	19	51	48	11	20	10	27	14

Matrix of mean similarities:

	UP. OHIO	CHES.-PO	SUSQUEHA	DELAWARE	L. CHES.	ROANCHOW	L. OHIO	UP. TENN
UP. OHIO	0.415	0.343	0.323	0.308	0.281	0.242	0.319	0.281
CHES.-PO	0.000	0.364	0.327	0.330	0.303	0.239	0.292	0.259
SUSQUEHA	0.000	0.000	0.385	0.392	0.267	0.196	0.253	0.247
DELAWARE	0.000	0.000	0.000	0.426	0.268	0.195	0.235	0.216
L. CHES.	0.000	0.000	0.000	0.000	0.371	0.262	0.265	0.205
ROANCHOW	0.000	0.000	0.000	0.000	0.000	0.290	0.226	0.178
L. OHIO	0.000	0.000	0.000	0.000	0.000	0.000	0.268	0.240
UP. TENN	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.293

Number of between and within similarities = 16594 3306

Weighted within-groups mean similarity, Wbar = 0.357
Unweighted within-groups mean = 0.362
Between-groups mean similarity, Bbar = 0.286

Observed ratio, M = Bbar/Wbar = 0.802
Observed difference, (Wbar-Bbar) = 0.706E-01

Starting 10000 randomly-sampled permutations.
Random Seed = -936915106

Random-sampling permutation test finished

Number of random trials = 10000

Number of trials with [M < (Observed M)] = 0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] = 0
For (Wbar-Bbar), estimated P-value =< 0.0001

These results are summarized in Figure 2C of the manuscript.

RESULTS FOR ANCESTRAL CATCHMENTS: ALL SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

Catchment descriptions:

ALBERMAR: greater Albermarle R. catchments (corresponding approximately to the Roanoke--Chowan
system)
CHESBAY: greater Chesapeake Bay (incl. Susquehanna, Potomac, smaller Chesapeake Bay
catchments plus the Lower Chesapeake grouping from the catchment classification scheme
identified previously)
DELAWARE: Delaware R. catchment,
LAURENT: Laurentian catchment (Upper Ohio tributaries identified above)
TEAYS: Teays R. catchment (incl. New--Kanawha, Sandy, and Guyandotte systems)
TENASI: Tennessee R. catchments

Run ID = Bray-Curtis similarity: Ancest. Drainage groups (9/99)
Number of sites = 200

Groups =	LAURENT	CHESBAY	DELAWARE	ALBERMAR	TEAYS	TANASI
Sizes =	19	119	11	10	27	14

Matrix of mean similarities:

	LAURENT	CHESBAY	DELAWARE	ALBERMAR	TEAYS	TANASI
LAURENT	0.307	0.232	0.251	0.142	0.212	0.165
CHESBAY	0.000	0.269	0.296	0.140	0.204	0.175
DELAWARE	0.000	0.000	0.388	0.123	0.195	0.174
ALBERMAR	0.000	0.000	0.000	0.173	0.141	0.094
TEAYS	0.000	0.000	0.000	0.000	0.183	0.161
TANASI	0.000	0.000	0.000	0.000	0.000	0.193

Number of between and within similarities = 12166 7734

Weighted within-groups mean similarity, Wbar = 0.257
Unweighted within-groups mean = 0.265
Between-groups mean similarity, Bbar = 0.203

Observed ratio, M = Bbar/Wbar = 0.788
Observed difference, (Wbar-Bbar) = 0.545E-01

Starting 10000 randomly-sampled permutations.
Random Seed = -936915563

Random-sampling permutation test finished

Number of random trials = 10000

Number of trials with [M < (Observed M)] = 0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] = 0
For (Wbar-Bbar), estimated P-value =< 0.0001

These results are summarized in Figure 2D of the manuscript.

RESULTS FOR ANCESTRAL CATCHMENTS: ALL SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

Catchment descriptions:

ALBERMAR: greater Albermarle R. catchments (corresponding approximately to the Roanoke--Chowan
system)
CHESBAY: greater Chesapeake Bay (incl. Susquehanna, Potomac, smaller Chesapeake Bay
catchments plus the Lower Chesapeake grouping from the catchment classification scheme
identified previously)
DELAWARE: Delaware R. catchment,
LAURENT: Laurentian catchment (Upper Ohio tributaries identified above)
TEAYS: Teays R. catchment (incl. New--Kanawha, Sandy, and Guyandotte systems)
TENASI: Tennessee R. catchments

Run ID = Dice (Sorensen) similarity: Ancest. Drainage groups (9/99)
Number of sites = 200

Groups =	LAURENT	CHESBAY	DELAWARE	ALBERMAR	TEAYS	TANASI
Sizes =	19	119	11	10	27	14

Matrix of mean similarities:

	LAURENT	CHESBAY	DELAWARE	ALBERMAR	TEAYS	TANASI
LAURENT	0.415	0.324	0.308	0.242	0.319	0.281
CHESBAY	0.000	0.332	0.344	0.225	0.271	0.245
DELAWARE	0.000	0.000	0.426	0.195	0.235	0.216
ALBERMAR	0.000	0.000	0.000	0.290	0.226	0.178
TEAYS	0.000	0.000	0.000	0.000	0.268	0.240
TANASI	0.000	0.000	0.000	0.000	0.000	0.293

Number of between and within similarities = 12166 7734

Weighted within-groups mean similarity, Wbar = 0.332
Unweighted within-groups mean = 0.331
Between-groups mean similarity, Bbar = 0.278

Observed ratio, M = Bbar/Wbar = 0.838
Observed difference, (Wbar-Bbar) = 0.539E-01

Starting 10000 randomly-sampled permutations.
Random Seed = -936915190

Random-sampling permutation test finished

Number of random trials = 10000

Number of trials with [M < (Observed M)] = 0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] = 0
For (Wbar-Bbar), estimated P-value =< 0.0001

These results are summarized in Figure2D of the manuscript.

RESULTS FOR STREAM ORDER: ALL SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

```
Run ID = Bray-Curtis similarity: Stream Order (9/99)
Number of sites = 200


Groups =     1         2         3
Sizes  =    68        72        60

Matrix of mean similarities:
           1       2       3
1      0.382   0.272   0.139
2      0.000   0.261   0.182
3      0.000   0.000   0.168

Number of between and within similarities =  13296  6604

Weighted within-groups mean similarity, Wbar =    0.274
Unweighted within-groups mean =    0.278
Between-groups mean similarity, Bbar = 0.202

Observed ratio, M = Bbar/Wbar = 0.736
Observed difference, (Wbar-Bbar) = 0.724E-01

Starting    10000 randomly-sampled permutations.
 Random Seed =  -936915635

Random-sampling permutation test finished

Number of random trials =    10000

Number of trials with [ M < (Observed M)] =        0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =        0
For (Wbar-Bbar), estimated P-value =< 0.0001
```

These results are summarized in Figure 2E of the manuscript.

RESULTS FOR STREAM ORDER: ALL SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

```
Run ID = Dice (Sorensen) similarity: Stream Order (9/99)
Number of sites = 200


Groups =     1         2         3
Sizes  =    68        72        60

Matrix of mean similarities:
           1       2       3
1      0.349   0.291   0.218
2      0.000   0.342   0.316
3      0.000   0.000   0.340

Number of between and within similarities =  13296  6604

Weighted within-groups mean similarity, Wbar =    0.343
Unweighted within-groups mean =    0.344
Between-groups mean similarity, Bbar = 0.276

Observed ratio, M = Bbar/Wbar = 0.805
Observed difference, (Wbar-Bbar) = 0.670E-01

Starting    10000 randomly-sampled permutations.
 Random Seed =  -936915280

Random-sampling permutation test finished

Number of random trials =    10000

Number of trials with [ M < (Observed M)] =        0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =        0
For (Wbar-Bbar), estimated P-value =< 0.0001
```

These results are summarized in Figure 2E of the manuscript.

RESULTS FOR TAXONOMIC CLUSTERS: REFERENCE SITES

BRAY-CURTIS DISSIMILARITY COEFFICIENT

```
Cluster Descriptions:

BC1:  predominantly blacknose dace
BC2:  predominantly brook trout
BC5:  predominantly blacknose dace + white sucker + longnose dace + other species
BC6:  predominantly slimy sculpin + brook trout + white sucker + other species
BC7:  white sucker + stoneroller + rock bass + blacknose dace + other taxa


 Run ID = Bray-Curtis similarity: B-C Clusters (ref sites) 9/99
 Number of sites =  30


 Groups =   1          5          6          7          2
 Sizes  =   5         11          2          8          4

 Matrix of mean similarities:
                1       5       6       7       2
       1   0.778   0.415   0.008   0.031   0.085
       5   0.000   0.467   0.068   0.147   0.274
       6   0.000   0.000   0.600   0.049   0.180
       7   0.000   0.000   0.000   0.236   0.084
       2   0.000   0.000   0.000   0.000   0.560

 Number of between and within similarities =    335   100

 Weighted within-groups mean similarity, Wbar =    0.479
 Unweighted within-groups mean =    0.440
 Between-groups mean similarity, Bbar = 0.171

 Observed ratio, M = Bbar/Wbar = 0.357
 Observed difference, (Wbar-Bbar) = 0.308

 Permutation test not done.
```

These results are summarized in Figure 3A of the manuscript.

RESULTS FOR TAXONOMIC CLUSTERS: REFERENCE SITES

DICE-SØRENSEN DISSIMILARITY COEFFICIENT

```
Cluster descriptions:

DS1:  predominantly blacknose dace
DS2:  predominantly blacknose dace and creek chub
DS3:  white sucker + creek chub + blacknose dace + other taxa
DS6:  predominantly brook trout and slimy sculpin
DS7:  blacknose dace + fantail darter + other taxa
DS8:  white sucker + stoneroller + blacknose dace + other taxa


 Run ID = Dice similarity: 6 HUC groups (ref sites) 9/99
 Number of sites =  30


 Groups =    1         7         6         3         2         8
 Sizes  =    3         6         4         8         2         7

 Matrix of mean similarities:
               1       7       6       3       2       8
       1   1.000   0.403   0.000   0.182   0.450   0.090
       7   0.000   0.437   0.250   0.304   0.407   0.221
       6   0.000   0.000   0.405   0.220   0.120   0.197
       3   0.000   0.000   0.000   0.520   0.379   0.414
       2   0.000   0.000   0.000   0.000   0.571   0.137
       8   0.000   0.000   0.000   0.000   0.000   0.469

 Number of between and within similarities =    361    74

 Weighted within-groups mean similarity, Wbar =    0.527
 Unweighted within-groups mean =    0.499
 Between-groups mean similarity, Bbar = 0.265

 Observed ratio, M = Bbar/Wbar = 0.502
 Observed difference, (Wbar-Bbar) = 0.263

 Permutation test not done.
```

These results are summarized in Figure 3A of the manuscript.

RESULTS FOR ECOREGION GROUPS: REFERENCE SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

```
Ecoregion groups:

BLUE RDG: Blue Ridge
C. APPS:  Central Appalachian Plateau
L-D VAL:  Limestone-dolomite valleys
N. APPS:  Allegheny Plateau
SND RDG:  Sandstone ridges
SHL RDG:  Shale Ridges
SHL VAL:  Shale valleys


 Run ID = Bray-Curtis similarity: Ecoregion groups (ref sites) 9/99
 Number of sites =  31


 Groups =     SHL RDG   N. APPS   SND RDG   SHL VAL   L-D VAL   BLUE RDG  C. APPS
 Sizes  =           6         2         5        10         4          2        2

 Matrix of mean similarities:
            SHL RDG N. APPS SND RDG SHL VAL L-D VAL BLUE RDG  C. APPS
 SHL RDG      0.252   0.300   0.136   0.240   0.291   0.216     0.321
 N. APPS      0.000   0.397   0.187   0.333   0.412   0.215     0.156
 SND RDG      0.000   0.000   0.158   0.182   0.165   0.202     0.118
 SHL VAL      0.000   0.000   0.000   0.250   0.306   0.245     0.203
 L-D VAL      0.000   0.000   0.000   0.000   0.367   0.221     0.160
 BLUE RDG     0.000   0.000   0.000   0.000   0.000   0.031     0.289
 C. APPS      0.000   0.000   0.000   0.000   0.000   0.000     0.000

 Number of between and within similarities =    386    79

 Weighted within-groups mean similarity, Wbar =    0.230
 Unweighted within-groups mean =    0.244
 Between-groups mean similarity, Bbar = 0.233

 Observed ratio, M = Bbar/Wbar =  1.01
 Observed difference, (Wbar-Bbar) = -.289E-02

 Starting    10000 randomly-sampled permutations.
  Random Seed =  -936984406

 Random-sampling permutation test finished

 Number of random trials =    10000

 Number of trials with [ M < (Observed M)] =     5133
 For M, estimated P-value  = 0.5133

 Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =     5130
 For (Wbar-Bbar), estimated P-value =  0.5130
```

These results are not presented in the manuscript.

RESULTS FOR ECOREGION GROUPS: REFERENCE SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

```
Ecoregion groups:

BLUE RDG: Blue Ridge
C. APPS:  Central Appalachian Plateau
L-D VAL:  Limestone-dolomite valleys
N. APPS:  Allegheny Plateau
SND RDG:  Sandstone ridges
SHL RDG:  Shale Ridges
SHL VAL:  Shale valleys


 Run ID = Dice similarity: Ecoregion groups (ref sites) 9/99
 Number of sites =  31


 Groups =   SHL RDG   N. APPS   SND RDG   SHL VAL   L-D VAL   BLUE RDG  C. APPS
 Sizes  =         6         2         5        10         4          2        2

 Matrix of mean similarities:
            SHL RDG  N. APPS  SND RDG  SHL VAL  L-D VAL  BLUE RDG  C. APPS
 SHL RDG      0.271    0.323    0.162    0.290    0.275     0.290   0.344
 N. APPS      0.000    0.250    0.300    0.369    0.349     0.321   0.235
 SND RDG      0.000    0.000    0.350    0.299    0.277     0.272   0.124
 SHL VAL      0.000    0.000    0.000    0.362    0.414     0.306   0.231
 L-D VAL      0.000    0.000    0.000    0.000    0.465     0.290   0.145
 BLUE RDG     0.000    0.000    0.000    0.000    0.000     0.125   0.294
 C. APPS      0.000    0.000    0.000    0.000    0.000     0.000   0.000

 Number of between and within similarities =    386    79

 Weighted within-groups mean similarity, Wbar =    0.310
 Unweighted within-groups mean =    0.342
 Between-groups mean similarity, Bbar = 0.291

 Observed ratio, M = Bbar/Wbar = 0.938
 Observed difference, (Wbar-Bbar) = 0.193E-01

 Starting    10000 randomly-sampled permutations.
  Random Seed =  -936984128

 Random-sampling permutation test finished

 Number of random trials =    10000

 Number of trials with [ M < (Observed M)] =     2164
 For M, estimated P-value  = 0.2165

 Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =     2206
 For (Wbar-Bbar), estimated P-value =  0.2207
```

These results are not presented in the manuscript.

RESULTS FOR CATCHMENTS (Modified HUCs): REFERENCE SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

```
Catchment descriptions:

CHES.-PO:  Middle Chesapeake Bay and the Potomac R.
DELAWARE:  Delaware R.
L. CHES.:  Lower Chesapeake Bay (incl. the York, Rappahannock, and James rivers)
UP. OHIO:  Upper Ohio R. (including the Allegheny, Monongehela, Youghigheny, and Cheat
rivers
           and small tributaries to the upper Ohio River mainstem)
L. OHIO:   Lower Ohio R. (incl. the Kanawha and Big Sandy rivers)
SUSQUEHA:  Susquehanna R.


 Run ID = Bray-Curtis similarity: 6 HUC groups (ref sites) 9/99
 Number of sites =  29


 Groups =   CHES.-PO  SUSQUEHA  UP. OHIO  L. CHES.  L. OHIO
 Sizes  =          8         6         3        7         5

 Matrix of mean similarities:
            CHES.-PO  SUSQUEHA  UP. OHIO  L. CHES.  L. OHIO
 CHES.-PO      0.259     0.272     0.218    0.282     0.215
 SUSQUEHA      0.000     0.263     0.269    0.241     0.189
 UP. OHIO      0.000     0.000     0.234    0.180     0.197
 L. CHES.      0.000     0.000     0.000    0.322     0.233
 L. OHIO       0.000     0.000     0.000    0.000     0.247

 Number of between and within similarities =    329    77

 Weighted within-groups mean similarity, Wbar =    0.270
 Unweighted within-groups mean =    0.274
 Between-groups mean similarity, Bbar = 0.238

 Observed ratio, M = Bbar/Wbar = 0.880
 Observed difference, (Wbar-Bbar) = 0.324E-01

 Starting    10000 randomly-sampled permutations.
  Random Seed =  -936989895

 Random-sampling permutation test finished

 Number of random trials =    10000

 Number of trials with [ M < (Observed M)] =      883
 For M, estimated P-value  = 0.0884

 Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =      886
 For (Wbar-Bbar), estimated P-value =  0.0887
```

These results are summarized in Figure 3B of the manuscript.

RESULTS FOR CATCHMENTS (Modified HUCs): REFERENCE SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

```
Catchment descriptions:


CHES.-PO:  Middle Chesapeake Bay and the Potomac R.
DELAWARE:  Delaware R.
L. CHES.:  Lower Chesapeake Bay (incl. the York, Rappahannock, and James rivers)
UP. OHIO:  Upper Ohio R. (including the Allegheny, Monongehela, Youghigheny, and Cheat
rivers
           and small tributaries to the upper Ohio River mainstem)
L. OHIO:   Lower Ohio R. (incl. the Kanawha and Big Sandy rivers)
SUSQUEHA:  Susquehanna R.


 Run ID = Dice similarity: 6 HUC groups (ref sites) 9/99
 Number of sites =  29


 Groups =   CHES.-PO  SUSQUEHA  UP. OHIO  L. CHES.  L. OHIO
 Sizes  =          8         6         3        7         5

 Matrix of mean similarities:
            CHES.-PO  SUSQUEHA  UP. OHIO  L. CHES.  L. OHIO
 CHES.-PO      0.346     0.330     0.335    0.354     0.293
 SUSQUEHA      0.000     0.376     0.327    0.272     0.242
 UP. OHIO      0.000     0.000     0.276    0.261     0.293
 L. CHES.      0.000     0.000     0.000    0.419     0.290
 L. OHIO       0.000     0.000     0.000    0.000     0.260

 Number of between and within similarities =    329    77

 Weighted within-groups mean similarity, Wbar =    0.348
 Unweighted within-groups mean =    0.358
 Between-groups mean similarity, Bbar = 0.304

 Observed ratio, M = Bbar/Wbar = 0.874
 Observed difference, (Wbar-Bbar) = 0.437E-01

 Starting    10000 randomly-sampled permutations.
  Random Seed =  -936989040

 Random-sampling permutation test finished

 Number of random trials =    10000

 Number of trials with [ M < (Observed M)] =      400
 For M, estimated P-value  = 0.0401

 Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =      415
 For (Wbar-Bbar), estimated P-value =  0.0416
```

These results are summarized in Figure 3B of the manuscript.

RESULTS FOR STREAM ORDER: REFERENCE SITES

BRAY-CURTIS SIMILARITY COEFFICIENT

```
Run ID = Bray-Curtis similarity: Stream Order (ref sites) 9/99
Number of sites =  31


Groups =   1         3         2
Sizes  =  12         9        10

Matrix of mean similarities:
           1       3       2
1      0.333   0.179   0.218
3      0.000   0.273   0.241
2      0.000   0.000   0.225

Number of between and within similarities =    318   147

Weighted within-groups mean similarity, Wbar =    0.281
Unweighted within-groups mean =    0.285
Between-groups mean similarity, Bbar = 0.211

Observed ratio, M = Bbar/Wbar = 0.752
Observed difference, (Wbar-Bbar) = 0.697E-01

Starting    10000 randomly-sampled permutations.
 Random Seed =  -936984684

Random-sampling permutation test finished

Number of random trials =    10000

Number of trials with [ M < (Observed M)] =       18
For M, estimated P-value  = 0.0019

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =       20
For (Wbar-Bbar), estimated P-value =  0.0021
```

These results are summarized in Figure 3C of the manuscript.

RESULTS FOR STREAM ORDER: REFERENCE SITES

DICE-SØRENSEN SIMILARITY COEFFICIENT

```
Run ID = Dice similarity: Stream Order (ref sites) 9/99
Number of sites =  31


Groups =   1         3         2
Sizes  =  12         9        10

Matrix of mean similarities:
           1       3       2
1      0.352   0.216   0.227
3      0.000   0.424   0.384
2      0.000   0.000   0.344

Number of between and within similarities =    318   147

Weighted within-groups mean similarity, Wbar =    0.370
Unweighted within-groups mean =    0.367
Between-groups mean similarity, Bbar = 0.268

Observed ratio, M = Bbar/Wbar = 0.724
Observed difference, (Wbar-Bbar) = 0.102

Starting    10000 randomly-sampled permutations.
 Random Seed =  -936984306

Random-sampling permutation test finished

Number of random trials =    10000

Number of trials with [ M < (Observed M)] =        0
For M, estimated P-value <= 0.0001

Number of trials with [(Wbar-Bbar) > Observed (Wbar-BBar)] =        0
For (Wbar-Bbar), estimated P-value =< 0.0001
```

These results are summarized in Figure 3C of the manuscript.